Association between serological salmonella monitoring in breeding herds and meat-juice prevalence in sow herds with production of finishers

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Introduction

Several epidemiological studies have studied risk factors for salmonella infections in finisher pigs. Most of these studies have focused on the risk for having a high prevalence, measured either bacteriologically or serologically.
Surveillance programs have been implemented in several European countries, measuring the salmonella prevalence in meat-juice samples. The rationale is that herds should decrease the salmonella prevalence by instituting salmonella reducing production and management strategies, including hygiene, all in-all out production and manipulating the gut flora by the use of organic acids, fermented liquid feed and coarse ground, non-pelleted feed.
Little emphasis has so far been put on the importance of spreading salmonella from herd to herd by the transport of pigs, be it gilts and boars for breeding or weaners and growers for finisher production.
This study investigates the effect of introducing gilts or boars from nucleus and multiplier herds with differing salmonella prevalences into sow herds with a production of finisher pigs.

Material and Methods

Data were collected in 3 different but overlapping time periods from two groups of herds, herds selling gilts and boars and sow herds with own production of finisher pigs for slaughter (integrated sow herds).
Integrated sow herds were divided into two groups based on microbiological results in 2007, herds with an isolation of Salmonelle Typhimurium from pen fecal samples, and herds without isolation of S. Typhimurium.
Serological results from herds selling gilts were obtained from the Danish Zoonosis Register for 2008. 10 blood samples are taken each month from these herds, and analysed in the Danish MIX-ELISA.
For each gilt producing herd, a seroprevalence was calculated as the number of samples with an OD% above 20, dividided by the total number of samples.
From the Danish Movement Database all herds receiving gilts or boars from the gilt producing herds in the period from July 1. 2008 to July 1. 2009, and the number of gilts and boars transported to the integrated sow herd from the gilt producing herd was calculated.
From the Danish Zoonosis register, results from meat-juice samples from the integrated sow herds were obtained for the period October 1. 2008 to September 30. 2009. To avoid the bias introduced by the Danish risk based surveillance, only the first sample taken each month was used in this study.
All integrated sow herds receiving gilts or boars from more than one gilt producer was excluded from the study.
The final data set included 158 gilt producers selling gilts or boars to 646 integrated sow herds.
Initial logistic regression analyses were done using Proc Glimmix (SAS Inst.), including the effect of gilt producer as a random effect, and handling overdispersion on the sow herd level by introducing a residual variation on the sow herd level as a random effect. The dependant variable was the proportion of positive meat juice samples per sow herd.
Two predictors and their possible interaction were investigated statistically. The effect of previous isolation of Typhimurium in the sow herd, and the effect of introducing pigs from gilt producers with different levels of Salmonella, measured as seroprevalence.
Several combinations and transformations of prevalence and number of gilts introduced were investigated, until a satisfactory and interpretable model was found.
To further explore the results, proc nlmixed (SAS Institute) was used to model a zero-inflated model. The code used for the model was modified from Stevenson (2005).
In the zero-inflated model, risk factors can be modelled for two different risks at the same time, the risk of being a positive herd and the risk of having a higher prevalence if positive.
This provides valuable information on the mechanisms affecting the salmonella level in pig herds.

Results

55 (8.5 %) of the sow herds had a positive pen fecal sample in 2007. 5634 meat juice samples were found from the sow herds. 302 meat juice samples were positive.

The best and most interpretable model for the effects of prevalence in the gilt producing herd and number of gilts or boars transported to the sow herd was obtained by calculating the number of seropositive gilts or boars being introduced by multiplying the number of gilts or boars transported by the prevalence from the salmonella surveillance from the gilt producer: Number of salmonella seropositive gilts or boars introduced (referred to as salmonella positive gilts)=Prevalence in gilt producing herd*number of gilts moved to the sow herd.

The final logistic regression model had the following form:

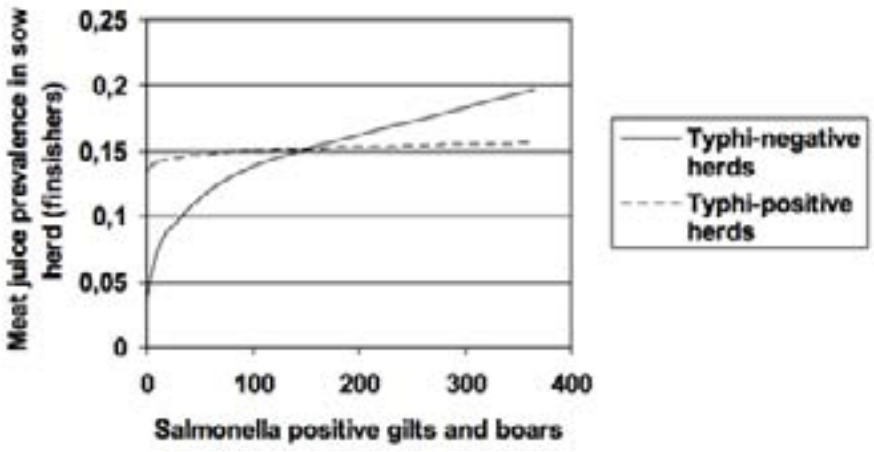
Logit (y/n)=$\alpha+\beta_1$*logN(salmonellapositive gilts+1) + β_2*(positive pen fecal sample in 2007) + β_3*interaction between the two predictors+γ*sow herd+residual variation (1 is added to number of salmonella positive gilts to avoid problems taking the logarithm).

The interaction between the two predictors was significant (p=0.02). For ease of reading, the table is broken up into sow herds with and without salmonella positive pen fecal samples in 2007. The OR for gilts moved into the herd is presented as the OR for doubling the number of positive gilts.

Table 1 summarizes the results from the logistic regression model, and figure 1 displays the results graphically.

The effect of salmonella positive gilts was significant (p=0.01) in sow herds without isolation of Typhimurium in 2007, but insignificant in sow herds with isolation of Typhimurium (p=0.79).

Figure 1. Results from logistic regression model (Glimmix).



There is little or no effect of introducing negative gilts into positive sow herds, whereas there is a clear efffect of introducing positive gilts into herds without isolation of S. Typhimurium in 2007.

Introducing more salmonella positive gilts and boars into the herd increases the prevalence of positive meat-juice samples in finisher herds from the integrated sow herd.

The results from the zero-inflated models are also presented in table 1, following the same procedure as for the logistic regression model. Figure 2 and 3 presents the results graphically for the zero-inflated model.

The risk of being a positive herd is not influenced by introducing positive gilts into an integrated sow herd (p=0.86), where S. Typhimurium already has been diagnosed, whereas the risk of becoming a positive sow herd increases considerably with the number of positive gilts introduced into herds where S. Typhimurium had not been diagnosed the preceeding year (p=0.02).

The association between prevalence in positive sow herds and introduction of positive gilts is much weaker. For sow herds with previous isolation of Typhimurium the effect was far from being significant (p=0.55), but for herds with no previous isolation, the effect was significant (p=0.03), although relatively small.

Figure 2. Risk for being a positive sow herd depending on number of salmonella positive gilts and boars introduced to an integrated sow herd.

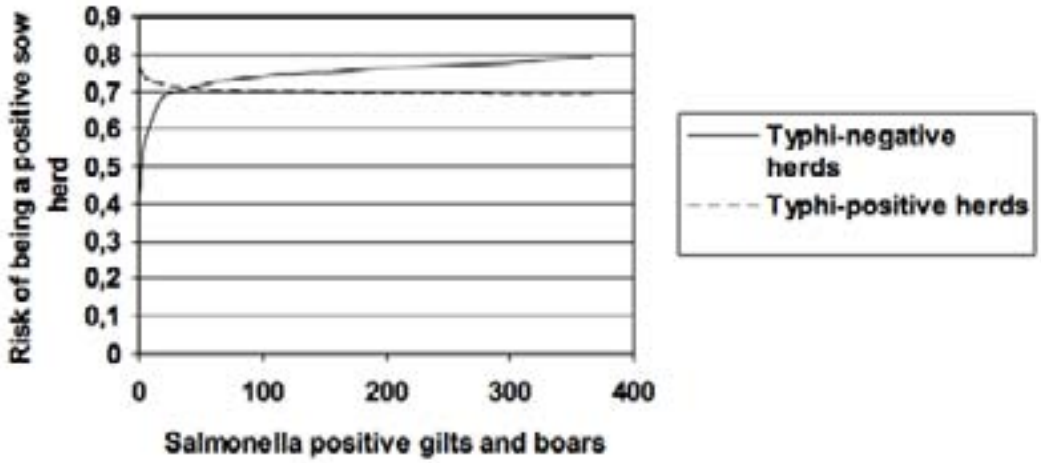


Figure 3. Association between prevalence in positive sow herds and number of salmonella seropositive gilts and boars introduced to an integrated sow herd

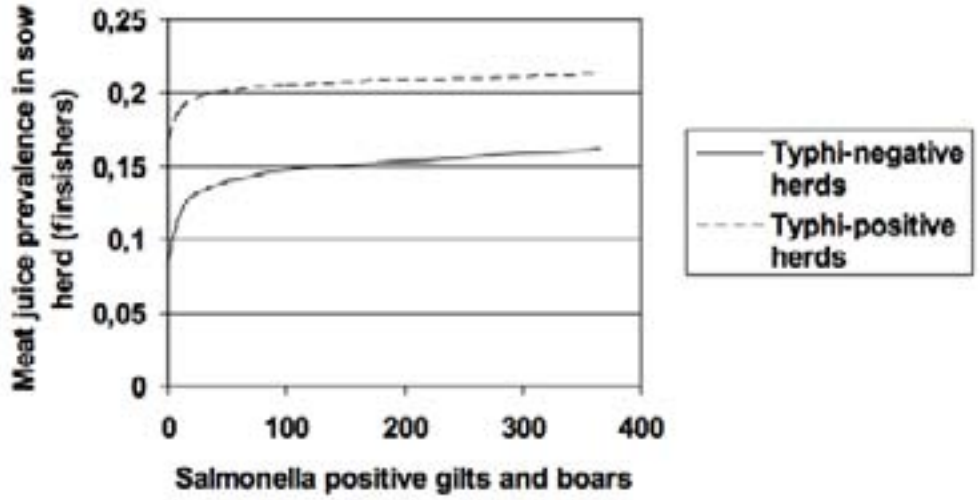


Table 1. Results from logistic regression models

	Sow herds without isolation of Typhimurium in 2007		Herds with isolation of Typhimurium in 2007	
Glimmix model	Estimate (CL)	OR (CL)	Estimate (CL)	OR (CL)
Intercept	-3.33		-1.89	
Log(salpos. gilts+1)*	0.33(0.20-0.45)	1.3(1.2-1.4)	0.03(-0.20-0.27)	1.02(0.9-1.2)
Zero-inflated model +/- part				
Intercept	-0.41		1.1621	
Log(salpos.gilts+1)*	0.37(0.07-0.68)	1.3(1.1-1.6)	-0.05(-0.61-0.51)	-1.0(0.7-1.4)
Zero-inflated model prevalence part				
Intercept	-2.44		-1.64	
Log(salpos.gilts+1)*	0.17(0.02-0.32)	1.1(1.0-1.3)	0.07(-0.17-0.31)	1.0(0.9-1.2)

**OR calculated as $2^{estimate}$, so it expresses the OR for doubling number of positive gilts introduced.*

Discussion

A relatively high number of sow herds were positive even when they did not receive gilts or boars from salmonella positive gilt producers. This probably reflects historic introductions into the sow herds before the observation period in this study, or introduction from other sources of infection.

The majority of sow herds were not sampled microbiologically in 2007, so the sow herds without an isolation of S. Typhimurium constitute a mixture of salmonella positive herds and salmonella negative herds, whereas sow herds with a positive S. Typhimurium isolation are positive.

This bias will most probably lead to an underestimation of the effect of bringing in positive gilts to a negative sow herd.

The fact that there was no effect of introducing salmonella positive gilts into sow herds with previous isolation of Typhimurium stresses the importance of protecting negative herds, if a reduction strategy for Salmonella has to be successful.

The risk of becoming a positive sow herd increases relatively fast with an increasing number of salmonella positive gilts. Herds that buy in replacement gilts will often introduce a much higher number of gilts than the relatively low number of gilts needed to pose a risk for the sow herd.

In this study 65 % of sow herds introduced more than 50 gilts pr year. If these gilts come from a positive gilt producer, then even at a relatively low prevalence, a high number of seropositive gilts will be introduced to the sow herd, almost inevitably infecting the sow herd.

Effectively this means that gilt producers should be declared as positive or negative, and negative sow herds should only get their replacement gilts from negative herds.

For positive sow herds little seems to be gained by restricting the introduction of positive gilts. And if a high number of sow herds are already positive, then the over all effect of restrictions on the gilt producer's trade will be limited, unless it is possible to eradicate salmonella from the positive sow herds. A strategy that so far has been shown to be very difficult without depopulation of the sow herd.

Conclusion

Introducing gilts from salmonella positive gilt producers poses a risk for becoming a positive sow herd, whereas the quantitative relation between seroprevalence in positive sow herds and introducing a high number of seropositive gilts is relatively weak.

Introducing seropositive gilts into a sow herd that already is positive, measured as a S. Typhimurium-positive pen fecal sample the previous year had little or no effect on the prevalence in the sow herd.

References

Stevenson, J. D., Bergerud, W. A., Ott, P. K. Analysis of presence/absence data when absence is uncertain (false zeroes): An example for the Northern Flying Squirrel using SAS. Extension note 74, July 2005.